

SEQUENCE LISTING

<110> GIMENO, Ruth

<120> METHODS FOR THE TREATMENT OF METABOLIC DISORDERS, INCLUDING OBESITY AND DIABETES

<130> MNI-220

<150> 60/271,655

<151> 2001-02-26

<160> 16

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44)...(1129)

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Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser Leu Glu Gln Ala
5 10 15 20

aac cgc acc cgc ttt ccc ttc ttc tcc gac gtc aag ggc gac cac cgg 151
Asn Arg Thr Arg Phe Pro Phe Ser Asp Val Lys Gly Asp His Arg
25 30 35

ctg gtg ctg gcc gcg gtg gag aca acc gtg ctg gtg ctc atc ttt gca 199
Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val Leu Ile Phe Ala
40 45 50

gtg tcg ctg ctg ggc aac gtg tgc gcc ctg gtg ctg gtg gcg cgc cga 247
Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu Val Ala Arg Arg
55 60 65

cga cgc cgc ggc gcg act gcc tgc ctg gta ctc aac ctc ttc tgc gcg 295
Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn Leu Phe Cys Ala
70 75 80

gac ctg ctc ttc atc agc gct atc cct ctg gtg ctg gcc gtg cgc tgg 343
Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu Ala Val Arg Trp
85 90 95 100

act gag gcc tgg ctg ctg ggc ccc gtt gcc tgc cac ctg ctc ttc tac 391
Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His Leu Leu Phe Tyr
105 110 115

gtg atg acc ctg agc ggc agc gtc acc atc ctc acg ctg gcc gcg gtc 439
Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr Leu Ala Ala Val

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Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln Arg Gly Val Arg			
135	140	145	
ggt cct ggg cgg cg gcg cgg gca gtg ctg ctg gcg ctc atc tgg ggc			535
Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala Leu Ile Trp Gly			
150	155	160	
tat tcg gcg gtc gcc gct ctg cct ctc tgc gtc ttc ttt cga gtc gtc			583
Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe Phe Arg Val Val			
165	170	175	180
ccg caa cgg ctc ccc ggc gcc gac cag gaa att tcg att tgc aca ctg			631
Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser Ile Cys Thr Leu			
185	190	195	
att tgg ccc acc att cct gga gag atc tcg tgg gat gtc tct ttt gtt			679
Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp Val Ser Phe Val			
200	205	210	
act ttg aac ttc ttg gtg cca gga ctg gtc att gtg atc agt tac tcc			727
Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val Ile Ser Tyr Ser			
215	220	225	
aaa att tta cag atc aca aag gca tca agg aag agg ctc acg gta agc			775
Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg Leu Thr Val Ser			
230	235	240	
ctg gcc tac tcg gag agc cac cag atc cgc gtg tcc cag cag gac ttc			823
Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser Gln Gln Asp Phe			
245	250	255	260
cgg ctc ttc cgc acc ctc ttc ctc atg gtc tcc ttc ttc atc atg			871
Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser Phe Phe Ile Met			
265	270	275	
tgg agc ccc atc atc atc acc atc ctc ctc atc ctg atc cag aac ttc			919
Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu Ile Gln Asn Phe			
280	285	290	
aag caa gac ctg atc tgg ccg tcc ctc ttc ttc tgg gtg gtg gcc			967
Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe Trp Val Val Ala			
295	300	305	
ttc aca ttt gct aat tca gcc cta aac ccc atc ctc tac aac atg aca			1015
Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu Tyr Asn Met Thr			
310	315	320	
ctg tgc agg aat gag tgg aag aaa att ttt tgc tgc ttc tgg ttc cca			1063
Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys Phe Trp Phe Pro			
325	330	335	340
gaa aag gga gcc att tta aca gac aca tct gtc aaa aga aat gac ttg			1111
Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys Arg Asn Asp Leu			
345	350	355	
tcg att att tct ggc taa tttttcttta tagccgagtt tctcacacct			1159
Ser Ile Ile Ser Gly *			
360			

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 35 40 45
 Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
 50 55 60
 Val Ala Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
 65 70 75 80
 Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
 85 90 95
 Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
 100 105 110
 Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
 115 120 125
 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
 130 135 140
 Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
 145 150 155 160
 Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
 165 170 175
 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
 180 185 190
 Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
 195 200 205
 Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
 210 215 220
 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
 225 230 235 240
 Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
 245 250 255
 Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
 260 265 270
 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
 275 280 285
 Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
 290 295 300
 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
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 Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
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<212> DNA
<213> Homo sapiens

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gcctctggc tggtggcgcg ccgacgcgcg cgcggcgcga ctgcctgcct ggtactcaac 240
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gtgcacactgc agcgcggcgt gcgggggtcct gggccggcggg cgcgggcagt gctgcgtggcg 480
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attcctggag agatctcggt gatgtctct tttgttaatt tgaacttctt ggtgccagga 660
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tcctcttctt tctgggtggt ggccttcaca tttgtaattt cagccctaaa ccccatcctc 960
tacaacatga cactgtgcag gaatgagttt aagaaaattt tttgctgcattt ctggttccca 1020
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<220>
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<222> (195)...(1280)

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tcgatgaccc tcttgacagc cacgagcgcg cgcagctccg ccatcttccc ggacgcgtgg 180
gccccggcgcg cggc atg tcc cct gag tgt gca cag acg acg ggc cct ggt 230
Met Ser Pro Glu Cys Ala Gln Thr Thr Gly Pro Gly
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ccc tcg cac acc ctg gac caa gtc aat cgc acc cac ttc cct ttc ttc 278
Pro Ser His Thr Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe
15 20 25

tcg gat gtc aag ggc gac cac cgg ttg gtg ttg agc gtc gtg gag acc 326
Ser Asp Val Lys Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr
30 35 40

acc gtt ctg gga ctc atc ttt gtc gtc tca ctg ctg ggc aac gtg tgt 374
Thr Val Leu Gly Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys
45 50 55 60

gct cta gtg ctg gtg gcg cgc cgt cgg cgc cgt ggg gcg tca gcc agc 422

Ala	Leu	Val	Leu	Val	Ala	Arg	Arg	Arg	Arg	Gly	Ala	Ser	Ala	Ser		
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ctg	gtg	ctc	aac	ctc	tgc	gat	ttg	ctc	ttc	acc	agc	gcc	atc		470	
Leu	Val	Leu	Asn	Leu	Phe	Cys	Ala	Asp	Leu	Leu	Phe	Thr	Ser	Ala	Ile	
80					85						90					
cct	cta	gtg	ctc	gtc	gtg	cgc	tgg	act	gag	gcc	tgg	ctg	ttg	ggg	ccc	518
Pro	Leu	Val	Leu	Val	Val	Arg	Trp	Thr	Glu	Ala	Trp	Leu	Leu	Gly	Pro	
95					100						105					
gtc	gtc	tgc	cac	ctg	ctc	tac	gtg	atg	aca	atg	agc	ggc	agc	gtc		566
Val	Val	Cys	His	Leu	Leu	Phe	Tyr	Val	Met	Thr	Met	Ser	Gly	Ser	Val	
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acg	atc	ctc	aca	ctg	gcc	gcg	gtc	agc	ctg	gag	cgc	atg	gtg	tgc	atc	614
Thr	Ile	Leu	Thr	Leu	Ala	Ala	Val	Ser	Leu	Glu	Arg	Met	Val	Cys	Ile	
125					130						135				140	
gtg	cgc	ctc	cgg	cgc	ggc	ttg	agc	ggc	ccg	ggg	cg	act	cag	gcg		662
Val	Arg	Leu	Arg	Arg	Gly	Leu	Ser	Gly	Pro	Gly	Arg	Arg	Thr	Gln	Ala	
145					150						155					
gca	ctg	ctg	gct	ttc	ata	tgg	gg	tac	tcg	g	ctc	gcc	g	ctg	ccc	710
Ala	Leu	Leu	Ala	Phe	Ile	Trp	Gly	Tyr	Ser	Ala	Leu	Ala	Ala	Leu	Pro	
160					165						170					
ctc	tac	atc	ttg	ttc	cgc	gtg	gtc	ccg	cag	cgc	ctt	ccc	ggc	gg	gac	758
Leu	Tyr	Ile	Leu	Phe	Arg	Val	Val	Pro	Gln	Arg	Leu	Pro	Gly	Gly	Asp	
175					180						185					
cag	gaa	att	ccg	att	tgc	aca	ttg	gat	tgg	ccc	aac	cgc	ata	gga	gaa	806
Gln	Glu	Ile	Pro	Ile	Cys	Thr	Leu	Asp	Trp	Pro	Asn	Arg	Ile	Gly	Glu	
190					195						200					
atc	tca	tgg	gat	gtg	ttt	ttt	gag	act	ttg	aac	ttc	ctg	gtg	ccg	gga	854
Ile	Ser	Trp	Asp	Val	Phe	Phe	Glu	Thr	Leu	Asn	Phe	Leu	Val	Pro	Gly	
205					210						215				220	
ctg	gtc	att	gtg	atc	agt	tac	tcc	aaa	att	tta	cag	atc	acg	aaa	gca	902
Leu	Val	Ile	Val	Ile	Ser	Tyr	Ser	Lys	Ile	Leu	Gln	Ile	Thr	Lys	Ala	
225					230						235					
tcg	cgg	aag	agg	ctt	acg	ctg	agc	ttg	gca	tac	tct	gag	agc	cac	cag	950
Ser	Arg	Lys	Arg	Leu	Thr	Leu	Ser	Leu	Ala	Tyr	Ser	Glu	Ser	His	Gln	
240					245						250					
atc	cga	gtg	tcc	caa	caa	gac	tac	cga	ctc	ttc	cgc	acg	ctc	ttc	ctg	998
Ile	Arg	Val	Ser	Gln	Gln	Asp	Tyr	Arg	Leu	Phe	Arg	Thr	Leu	Phe	Leu	
255					260						265					
ctc	atg	gtt	tcc	ttc	atc	atg	tgg	agt	ccc	atc	atc	atc	acc	atc		1046
Leu	Met	Val	Ser	Phe	Phe	Ile	Met	Trp	Ser	Pro	Ile	Ile	Ile	Thr	Ile	
270					275						280					
ctc	ctc	atc	ttg	atc	caa	aac	ttc	cg	cag	gac	ctg	gtc	atc	tgg	cca	1094
Leu	Leu	Ile	Leu	Ile	Gln	Asn	Phe	Arg	Gln	Asp	Leu	Val	Ile	Trp	Pro	
285					290						295				300	
tcc	ctt	ttc	ttc	tgg	gtg	gtg	gcc	ttc	acg	ttt	gcc	aac	tct	gcc	cta	1142
Ser	Leu	Phe	Phe	Trp	Val	Val	Ala	Phe	Thr	Phe	Ala	Asn	Ser	Ala	Leu	

305

310

315

aac ccc ata ctg tac aac atg tcg ctg ttc agg aac gaa tgg agg aag	1190
Asn Pro Ile Leu Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys	
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330	

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Ile Phe Cys Cys Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp	
335	340
345	

acg tct gtc agg cga aat gac ttg tct gtt att tcc agc taa	1280
Thr Ser Val Arg Arg Asn Asp Leu Ser Val Ile Ser Ser *	
350	355
360	

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<212> PRT

<213> Murine ortholog

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Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu	
50 55 60	
Val Ala Arg Arg Arg Arg Gly Ala Ser Ala Ser Leu Val Leu Asn	
65 70 75 80	
Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu	
85 90 95	
Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His	
100 105 110	
Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr	
115 120 125	
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg	
130 135 140	
Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala	
145 150 155 160	
Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Tyr Ile Leu	
165 170 175	
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro	
180 185 190	
Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp	
195 200 205	
Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val	
210 215 220	
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg	
225 230 235 240	
Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser	
245 250 255	
Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser	
260 265 270	
Phe Phe Ile Met Trp Ser Pro Ile Ile Thr Ile Leu Ile Leu	

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Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe		
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Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu		
305	310	315
Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys		
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Arg Asn Asp Leu Ser Val Ile Ser Ser		
355	360	

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tacaacatgt cgctgttcag gaacgaatgg aggaagattt tttgctgtt cttttttcca 1020
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<400> 7
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<210> 9
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<400> 9

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